Probe

Newsletter for the USDA Plant Genome Research Program

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Edible Vaccines

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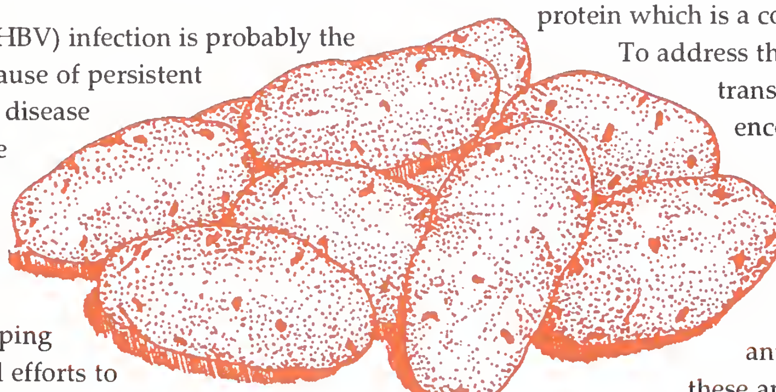
Vaccines are primary tools in programs for health intervention for both humans and animals. They would be more widely used—especially in developing countries—if their cost of production could be reduced and if they could be distributed without refrigeration. Research underway is dedicated to solving these limitations by finding ways to produce oral (edible) vaccines in transgenic plants.

Hepatitis B virus (HBV) infection is probably the single most important cause of persistent viremia in humans. The disease is characterized by acute and chronic hepatitis, which can also initiate hepatocellular carcinoma. The prevalence of this disease in developing countries justified initial efforts to express HBV candidate vaccines in plants.

Currently, two forms of HBV vaccines are available, both of which are injectable and expensive: one purified from the serum of infected individuals and the other a recombinant antigen expressed and purified from yeast. We have transformed plants with the gene encoding the hepatitis B surface antigen (HBsAg); this is the same antigen used in the commercial yeast-derived vaccine.



An antigenic spherical particle was recovered from these plants which is analogous to the recombinant hepatitis surface antigen (rHBsAg) derived from yeast. Parenteral immunization of mice with the plant-derived material has demonstrated that it retains both B- and T-cell epitopes, as compared to the commercial vaccine.

Diarrheal disease causes up to 10 million deaths per year in the developing world, primarily among children. Relatively little research on vaccines to prevent these diseases is underway, as they represent more of a nuisance than a severe problem in developed countries. Studies supported by the World Health Organization have demonstrated an effective vaccine for cholera, which provides cross-protection against enterotoxic *Escherichia coli*. This vaccine is not available, however, in large part due to cost of production of the bacterial toxin protein which is a component of its formulation.

To address this limitation, plants were transformed with the gene encoding the B subunit of the *E. coli* heat labile enterotoxin (LT-B). Transgenic potatoes expressing LT-B were found to induce both serum and secretory antibodies when fed to mice; these antibodies were protective in bacterial toxin assays *in vitro*. This is the first "proof of concept" for the edible vaccine.

The selection of a plant system for delivery of edible vaccines for humans has been addressed. Recognizing that it is necessary to express the desired protein in a food that is consumed raw (to avoid denaturation of the candidate vaccine protein), a system to transform banana plants has been developed. Bananas are produced in

most developing countries and are fed uncooked to infants and adults. The expression of candidate vaccines in banana fruit will be dependent upon identification of suitable tissue-specific promoters to drive the desired gene expression. Research to find these genetic regulatory elements is now underway.

Edible vaccine research is currently directed at human diseases, with a special emphasis on the developing world. The technology will also have immediate value for the production of inexpensive vaccines as feed additives for agricultural animals. Since various plant tissues are fed to animals, other plants such as alfalfa, maize and wheat could be valuable vehicles to deliver vaccines (and perhaps other pharmaceuticals) for the betterment of animal health.

(Charles Arntzen's research on vaccine development is supported in part by grants from the Thrasher Foundation, the USDA Competitive Grants Program, and the National Institutes of Health (NIH). Mary Blake's research is supported by the Clayton Foundation for Research.)

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Weeds World *Arabidopsis* Newsletter on WWW

A new electronic newsletter, ***Weeds World***, premiered in November 1994. Endorsed by the Arabidopsis community, *Weeds World* is intended as a popular forum for information exchange, in the way that the *Worm Breeders Gazette* has served the *C. elegans* community. The newsletter will be published in April, August and December of each year.

Weeds World can be accessed on a constant basis through these World-Wide Web (WWW) servers: the AAtDB WWW server at Nottingham (UK), and the Agricultural Genome WWW Server at the National Agricultural Library (NAL), Beltsville (USA). In addition, the newsletter is on the Gopher server AAtDB Research Companion at Massachusetts General Hospital (MGH), Boston (USA). It can be searched in the same way as one can currently search AAtDB, the *arab-gen* bulletin board postings, and the Nottingham Seed List.

The electronic newsletter is WAIS indexed, and future issues will also be linked as closely as possible for easy tracking of scientific developments.

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André Named NAL Director

Photo by Joseph Swab

Pamela Q.J. André has been named Director of the National Agricultural Library (NAL), replacing Joseph H. Howard, who retired on February 3, 1994.

André has served in various library management positions with the Federal Government over a 28-year career. She had been acting NAL director since Howard's retirement.

From 1984 until her designation as acting NAL director, André had been NAL's Associate Director for Automation. In this position, she guided NAL's program to apply electronic technology to library operations. In particular, she was instrumental in the success of the National Agricultural Text Digitizing Program, in which selected portions of the NAL collection were placed on compact discs and distributed to land-grant university libraries nationwide. She also led the library's efforts to make NAL services and products available on the Internet.

"As the acting director and an NAL associate director, André has admirably demonstrated her leadership abilities," said Dean Plowman, USDA's Acting Assistant Secretary, Science and Education. "She has been instrumental in steering the library in the direction of becoming electronically accessible, worldwide. We are confident that she will continue this exemplary service as the NAL director."

Prior to joining NAL, André held a variety of positions with the Library of Congress (LC). As a computer systems analyst, she worked on developing LC's bibliographic computer system. She was later the Assistant Chief of the MARC Editorial Division. In 1982, she was named to the management team for the LC Optical Disk Pilot Project.

She has served on the editorial boards of several library-related publications and is a member of the American Library Association and the International Association of Agricultural Information Specialists.

André has a master's degree in library science from the University of Maryland. Her articles on library automation have appeared in numerous publications, and she is a popular speaker on the uses of electronic technologies in libraries.

The National Agricultural Library is the largest agricultural library in the world, with over 2.1 million volumes and receiving 22,000 periodicals annually. It is one of three national libraries of the United States, along with the Library of Congress and the National Library of Medicine. ◆

Probe

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National Agricultural Library

Probe

Weeds World-cont. from page 2

Weeds World will include short reports, short papers and slightly longer pieces similar to those in the AIS (*Arabidopsis* Information Service). Articles can be the approximate length of a conference abstract (500 words) and preferably no longer than one page, excluding figures. They need not be as formal as the above examples, and can be brief outlines of lab research interests, or background to current work.

The newsletter also will feature the following items: abstracts from papers; information about upcoming meetings, conferences and courses; tips and protocols for technical procedures; announcements from *Arabidopsis* Biological Resource Center (ABRC) and Nottingham *Arabidopsis* Stock Centre (NASC) about new stocks, informatics developments and policy decisions; genetic maps and gene lists; job announcements; and humorous trivia and/or cartoons.

To read the newsletter, use the following WWW URL to connect to the server nearest you:

- http://nasc.nott.ac.uk:8300 (Nottingham, UK)
- http://weeds.mgh.harvard.edu/weedsworld/home.html (MGH, Boston, MA, USA)
- http://probe.nalusda.gov:8300/aboutaatdb.html (NAL, Beltsville, MD, USA)

Readers who wish to have a print copy may download and print out a text version of *Weeds World* from the *AAtDB Research Companion*.

The newsletter will be produced by Mary Anderson, Sam Cartinhour, John Morris and Randy Scholl. Queries should be sent to:

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Touching Base with Mary Polacco

Major New Data in MaizeDB and How To Access

Mary Polacco, Database Developer
Plant Genetics Research, ARS, USDA
University of Missouri
Columbia, MO

The following data have been added to MaizeDB since summer 1994:

1. QTL representation
2. Connection to GRIN
3. Connections to external databases
4. Allozyme variations
5. New Maps
6. Maize cDNAs, partially sequenced; GenoBase BLAST connections
7. How to access MaizeDB

1. Representation of Quantitative Trait Loci (QTL). Design has been completed and test data have been entered. On-line access to data that define QTL will facilitate comparisons with genome information obtained from classical, biochemical and molecular genetic studies. Traits where public information is available include yield and yield components, quality attributes, such as kernel protein and starch concentrations, developmental characteristics, and responses to pests and abiotic stress.

The design efforts, coordinated by Patrick Byrne of the Missouri MaizeDB development team, included consultations with maize breeders and extensive review of the literature. Special thanks are due Mary Berlyn and Stan Letovsky for assistance in design and implementation.

2. World Wide Web (WWW) Connection to Germplasm Resource Information Network (GRIN). MaizeDB Stocks (germplasm) records are now connected to their GRIN counterparts on the World Wide Web. To access the GRIN record, click on the GRIN KEY, listed

towards the bottom of a record. Special thanks are owed to Steve Beckstrom-Sternberg, USDA-ARS, for providing parsed GRIN data, and to Stan Letovsky for the GENERA-Sybase WWW gateway.

3. Connections to External Databases by WWW. Currently, records in 14 external databases are accessible from MaizeDB records using the WWW. Click on the KEY listed for the database for relevant external record; click on the database name to access the external database. Links to the correct external record are part of the data curation at Missouri.

Sequences

GenBank	Nucleotide sequences
dbEST cDNA	Partial, +-strand sequences, with similarity search results
GenoBase	Sequences, custom format, BLAST searching
SwissProt	Protein sequences, ProSite, MedLine, ENZYME; connects reversibly to MaizeDB Gene Products
PIR	Protein sequences
Prosite	Motifs
ENZYME	Click on the EC number for Gene Products that are enzymes; reactions, connections to SwissProt sequences for all enzymes with the same EC# and to OMIN for human diseases

Genomes, Stocks

E. coli, CGSC	Stocks, genes, maps, more
Arabidopsis, AAtDB	Genes, maps, more
Yeast, SacchDB	Genes, maps, more
RiceGenes	Genes, maps, more
GrainGenes	Genes, maps, more
XLocus	Genome comparison
GRIN	Germplasm (see above)

4. Allozyme Variations. These data were provided in electronic form by Charles Stuber and include both null alleles and electrophoretic variants for some 21 loci, as surveyed across 398 maize lines. Information about germplasm or stocks with characterized enzyme electrophoretic mobility variants or null alleles may be retrieved by typing in the "phenotype" field on the Stock form as follows:

PHENOTYPE: electro

or

PHENOTYPE: electrophoretic mobility

PHENOTYPE: null

5. Maps. Mycogen maps (365 markers)
CIMMYT maps (346 markers)
UMC 1995 RFLP maps (602 markers)

The UMC 95 maps and data were first made available prior to publication through the MaizeDB, and demonstrated at the Plant Genome III meeting in San Diego, CA. Marker sets for the map were provided by Mycogen Plant Science, Asgrow Seed, Brookhaven National Laboratory, California State University-Hayward; Native Plants Inc; Pioneer Hi-Bred International and the University of Missouri-Columbia. Individual clones were contributed by many other laboratories.

A. Map retrieval
To view the Mycogen or UMC maps, use the MAP form, and type in NAME field:

NAME: Mycogen
to retrieve all Mycogen maps
NAME: Mycogen%2
to retrieve Mycogen chromosome 2 map
NAME: umc 95
to retrieve all umc 95 maps
NAME: umc 95%2
to retrieve umc 95 chromosome 2 map

Several populations have been used for mapping at CIMMYT; to view all the CIMMYT maps, use the MAP form as above, but type at

SOURCE: CIMMYT

or, for chromosome 2 maps, type

SOURCE: CIMMYT
NAME: %2

B. Map Scores; Probes for the UMC 95 maps
A panel of the complete Map Scores for the umc 95 maps may be retrieved by WWW access: use the complex query form for "Mapping Population, Map Score" and select

PANEL TYPE: Immortal F2.

Many of the probes are available from the University of Missouri RFLP lab; please check MaizeDB

regarding availability. Our WWW server includes a Probe Request form. An improved core marker set has been defined and may be requested from Theresa Musket, musket@teosinte.agron.missouri.edu.

6. Maize cDNAs - Partial Sequences, Submitted to the dbEST Database of the NIH National Center for Biotechnology Information (NCBI).

Currently, these cDNAs are derived from shoot, endosperm or etiolated leaf libraries. These now number over 950 clones, and many have been mapped, either to a recombinant inbred mapping population or immortal F2s. Mapping data and probe details are stored in MaizeDB. Sequences are accessible, from the Probe, Locus or Allele records, using the WWW KEYS, automatically supplied to MaizeDB from dbEST.

A number of sequences, not yet submitted to GenBank, are stored at the University of Minnesota Plant Genome Informatics Center, and may be accessed indirectly from our home page or directly at URL: http://lenti.med.umn.edu/~shoop/sample.html

Probes with a GenoBase external database KEY are accessible to the BLAST searching engine at the NCBI, and will allow users to execute a new similarity search based on either deduced protein or nucleotide sequence.

7. Access - Access to the MaizeDB has grown exponentially, and now averages over 15,000 transactions/month, with about two-thirds over the WWW. Any record viewed may be e-mailed by users to themselves.

To connect on the World Wide Web (WWW) to the data, updated daily, the address or URL (uniform resource locator) is: http://www.agron.missouri.edu

This address also provides a direct link to the National Agricultural Library plant genome project, which provides MOULON-ACeDB access to the data for several plant genomes, including maize.

To connect by gopher: gopher.agron.missouri.edu and set port to: 70

Guest access to the robust queries permitted by the SYBASE APT forms is available:
telnet teosinte.agron.missouri.edu
login: guest
password: corncob

The guest login account also supports access to gopher and the WWW. Please download the tutorial, after you log in, for information on cursor action and scrolling, and for sample queries.

We welcome suggestions and questions:
db_request@teosinte.agron.missouri.edu

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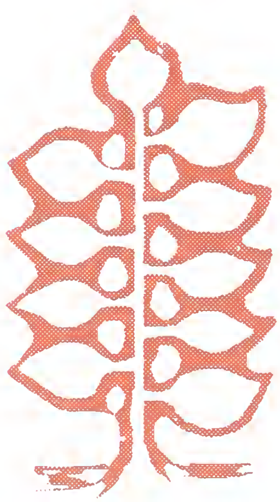
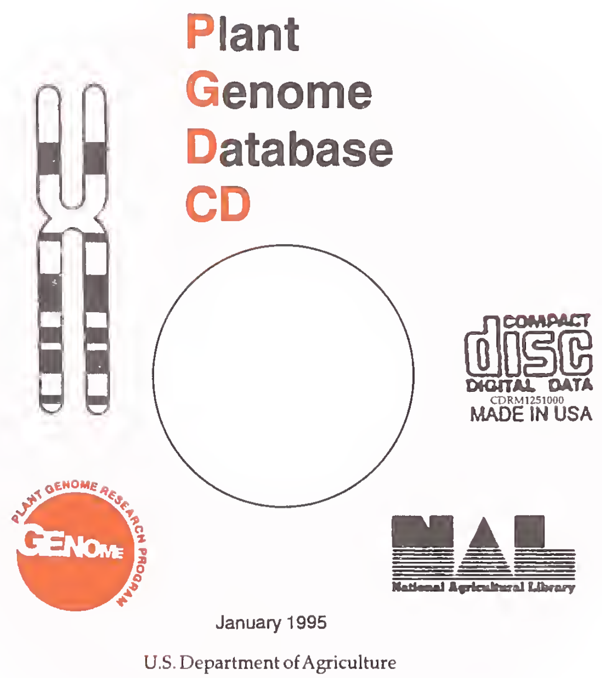


The PLANT GROWTH REGULATOR SOCIETY OF AMERICA (PGRSA) announces the appointment of Dr. Stephen J. Cutler as the new editor of the PGRSA Quarterly. Dr. Cutler is currently an Assistant Professor of Medicinal Chemistry in the School of Pharmacy, Mercer University, Atlanta, GA. Dr. Cutler's research interests are in the use of natural plant products and their derivatives as agrochemicals and pharmaceuticals.

New associate editors for the Quarterly will be Dr. Carole Bassett, USDA, ARS, Kearneysville, WV; Dr. Caula Beyl, Alabama A&M University, Normal, AL; Dr. Jim Metzger, The Ohio State University, Columbus, OH; and Dr. Duane Greene, University of Massachusetts, Amherst, MA. ◆

For those of you *not yet cruising* along the superhighway of information.



Check the appropriate box on the last page of this newsletter and mail it back to us with a self-addressed label. The Plant Genome Data and Information Center will gladly mail you a free CD.

There is a new release of the Plant Genome Database on CD. *Free of charge.*

Off the Wire

New CD-ROMs To Feature Asian Medicinal Databases

Two databases, one covering aromatic and medicinal plants; another featuring traditional practices in Oriental medicine, will become available on CD-ROM, according to announcements by their sponsoring research organizations.

The first is an integrated and factual database from the Asian Pacific Information Network on Medicinal and Aromatic Plants (APINMAP). Participants at the fourth APINMAP Management Board meeting (University Kebangsaan Malaysia, Bangi, Selangor Darul Ehsarn, Malaysia, June 21-23, 1994) made the decision to release it in CD-ROM format.

The APINMAP integrated database contains information on medicinal and aromatic plants in: agriculture and forestry; plant biology; chemistry and chemistry of natural products; pharmacy; health and medicine, including veterinary medicine; and ethnology. It also covers industrial applications; economics; policies and legislation; education, extension, and promotion; and general plant characteristics.

The factual database, on the other hand, provides users with data pertaining to five major areas of study on medicinal and aromatic plants: botany, chemistry, pharmacy, medicine, and marketing.

The CD-ROM undertaking is made possible through a grant given by the International Development Research Centre (IDRC) of Canada. The grant is part of a 6-year IDRC project called "CD-ROM of Asian Information on Health and Environment." APINMAP is one of the initial nine institutions which will be involved in contributing its data to the project. The Publication and Information Directorate (PID) in India is the project's lead agency.

APINMAP is a voluntary cooperative program established by the United Nations Educational, Scientific and Cultural Organization (UNESCO) in 1987. Its primary aim is to assist its participating countries in improving and enhancing their capabilities to collect, process, disseminate, and use research information and data on medicinal and aromatic plants. So far, the network has 14 member countries: Australia, China, India, Indonesia, South Korea, Malaysia, Nepal, Pakistan, Papua New Guinea, the Philippines, Sri Lanka, Thailand, Turkey, and Vietnam.

APINMAP's Network Center is SEAMEO SEARCA's Information Resources Unit (IRU, formerly Agricultural Information Bank for Asia or AIBA). IRU produces the APINMAP databases and distributes them to the national nodes of each member country, advises and arranges staff training, coordinates activities in accordance with the approved work plan of the network, and assists the Philippine-based Secretariat in disseminating information on APINMAP activities.

APINMAP's management board meets once every 2 years to discuss future activities and directions of the network. It is composed of representatives from the national nodes of each member country. During its meeting, the Board discusses policies which may affect the network in the future, including suspension of inactive members, full document backup to citations/ abstracted inputs, copyright protocol, pricing of APINMAP products, identified users, treatment of infor-

mation from unwritten sources, sale or distribution of database searches in diskettes, and training of staff in each national node.

In addition to the country representatives, the meeting was attended by Delia E. Torrijos, UNESCO Regional Adviser for the General Information Programme in Asia and the Pacific; Director Percy E. Sajise, Dr. Josephine C. Sison and Alice H. Rillo, IRU Project Officer and Information Specialist, respectively, all of SEARCA; and Dr. Narong Chomchalow, an observer from the Asian Network on Medicinal and Aromatic Plants (ANMAP).

The second database, focusing on traditional Oriental medicine, was developed at the Natural Products Research Institute, Seoul National University, Republic of Korea. It is an effort of the New Korean Drugs Research and Development Project, one of the national research projects supported by the Ministry of Science and Technology since 1992.

Called TradiMed, the database's content is derived from knowledge of traditional Chinese medicine. Its aim is to integrate the ancient wisdom of Oriental tradition with modern science and technology.

TradiMed offers three major information databases:

- a prescription database, which provides information on efficacy, dosages, adverse effects, and other knowledge about thousands of traditional Korean and Chinese drugs.
- a chemistry database, which includes thousands of natural constituents found in herbal, microbial, and marine sources, showing the chemical formula, chemical structure, and various analytical data, such as spectral data.
- a photo-image database, which shows full-color images of medicinal plants and herbs identified by systematic botanists.

TradiMed contains information useful to researchers searching for new drugs derived from natural products and traditional medicines. At present, domestic users are able to access the database through a national network. Special CD-ROM titles were slated to become available for the practices of Western and Oriental doctors and pharmacists at the end of 1994. Beginning this year, information in the database will be translated to English so that Western scientists can access it.

For more information, please contact the following address: Natural Products Research Institute, Seoul National University 28 Yeongun-Dong, Jongro-Ku Seoul 110-460 REPUBLIC OF KOREA

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Telex: SNUROK K29664
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Plant Genome III

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The third plant genome international conference on the status of plant genome research was held in San Diego, California, USA, on January 15-19, 1995. Plant Genome III presented the following areas of genome research and development: isolation and transformation of agriculturally important genes, comparative genetic mapping, chromosome structure, and new instrumentation and automation technology. Plenary and general sessions and specific workshops highlighted new computer tools, databases, nomenclature, gene-tagging for abiotic stress, or individual species: pine trees, *Arabidopsis*, barley, tree fruits, maize, legumes, cotton and grass genome integration.

The conference was sponsored and supported by the USDA Agricultural Research Service (ARS), the USDA National Agricultural Library (NAL), USDA Cooperative State Research, Education, and Extension Service, National Research Initiative Competitive Grants Office, John Innes Centre (UK), the Rockefeller Foundation, and the International Society for Plant Molecular Biology. The meeting attracted over 660 participants from 25 countries; there was substantially increased participation from the European Community and Japan.

The plant genome research program is now entering its fifth year. Jerome Miksche, Director, USDA Plant Genome Research Program, commended conference participants for their efforts leading to development of new genomic information, new technologies, and international collaboration. He stressed the need for continued and expanded funding to support ongoing research efforts. He indicated that the program, using molecular genetics to search for genes of agricultural importance and to construct detailed maps, has already yielded a plentiful harvest of new information.

Marker-Based Breeding

Genetic improvement of crop plants depends upon genetic diversity. Intensive breeding for crop improvement has narrowed the diversity of many of our commercially important cultivars. For these crop species, additional genetic improvement will be increasingly difficult to achieve without the new approaches to breeding now under development.

Steve Tanksley (Cornell University, USA) discussed the need to develop new QTLs, and identified a strategy for advanced backcross analysis: nearly elite lines are matched with an exotic, or ancient, donor germplasm. The F1 progeny are backcrossed several times and rapidly screened for advantageous QTLs. Tanksley's approach is to develop QTL isogenic lines for rapid map-based plant breeding.

Marker-facilitated QTL manipulation has been successfully used to transfer traits between elite maize lines, Charles Stuber (North Carolina State University, USA) reported. The marker-assisted backcrossing was used in a complex breeding program which greatly accelerated the development of a new hybrid line. The two highest yielding hybrids afforded an improvement of 1.7 to 1.9 ton/hectare.

A Tree Fruit Workshop, organized for the first time at the conference, also announced accelerated breeding. Norman Weeden (Cornell University, USA) reported that high heterozygosity, characteristic of the apple genomes and related species within the Rosaceae family, permits genetic analysis of isolated genes approximately 9 months after making a cross between two varieties. This technique can accelerate breeding by 5 to 15 years while reducing costs. Future breeding goals aim to develop cultivars with im-

proved fruit quality, as well as insect and disease resistance.

Maps with over 200 segregation markers for several major apple cultivars have already been completed. Weeden indicated that molecular techniques such as RAPD and RFLP markers and bulk segregant analysis are being incorporated into the apple breeding program at Cornell. Genes encoding fruit color, fruit size, columnar growth habit, bud break, scab resistance, powdery mildew, and aphid resistance have recently been isolated. The USDA plant genome mapping program has expanded its mapping efforts from a few species initially to over 45 species.

Genome mapping activities in citrus, peaches, almonds, cherries, and grapes by U.S. institutions and the European Community were presented and discussed. Several laboratories reported on the isolation of molecular markers for nematode-resistance. Identification of molecular markers near the nematode resistance gene(s) and generation of high-density maps in this region will enable scientists to develop new resistant plant cultivars.

Comparative Mapping

Tim Helentjaris (Pioneer Hi-Bred International, Inc., USA) presented insights into the evolutionary origins and the duplication of large segments of chromosome within the maize genome. He described how comparative mapping is distinguishing between alternative hypotheses of duplication: internal duplication with subsequent rearrangement, or by the fusion of two distinctive genomes. The development of comparative maps for individual species is allowing scientists to pool genetic information from related crop species, and is increasing the efficiency of molecular-marker and gene isolation technologies applied to crop improvement.

Comparative mapping applied to divergent taxa and to divergent chromosomes within a particular taxon can provide a better understanding of the evolution of a phenotype. Andrew Paterson (Texas A&M University, USA) showed that comparative mapping provides an opportunity to use chromosomal rearrangements as phylogenetic tools. A comparative approach to this problem will increase the number of available markers in any grass crop and will be useful for construction of a framework map of conserved regions in the genomes of the Gramineae family.

Mark Sorrells (Cornell University, USA) identified 150 anchor probes that hybridize to most of the targeted genomes; many of these probes were mapped in at least 5 species of the Gramineae family. Katrien Devos (John Innes Centre, Norwich, UK) showed the comparative maps of wheat, barley, and rye and concluded that arrangement of genes along the chromosomes of those cereal species is remarkably conserved. Devos predicts, on the basis of current data, that grass comparative genetics will use rice as the pivotal genome.

Comparative mapping is bringing scientists together who would otherwise have little in common: an international cross-species collaboration has been proposed for the Gramineae. The effort is being spearheaded by Jeff Bennetzen (Purdue University, USA) and Mike Gale (John Innes Institute, UK). The International Grass Genome Integration (IGGI) Program will, as noted above, use rice as the central genome for comparative mapping. Anchor probes will link genomes to map across species. Anchor probes are currently available for wheat vs. rice comparisons. Significant progress in identifying genes and rapidly transferring biochemical and physiological information is expected when mutants are mapped.

Mapping of Legume Genomes

Gary Kochert (University of Georgia, USA) compared the genomes of peanut and soybean. Several probes were tested in genomic blots of pea, alfalfa, soybean, and peanut for their usefulness in comparative mapping. Comparative mapping, Kochert said, will provide new and useful tools to locate genes encoding valuable agronomic traits. Norman Weeden (Cornell University, USA) reported considerable conservation of gene linkage of the agriculturally important pea subfamily. Detailed genetic maps consisting of hundreds of molecular markers are needed for positional cloning of genes and map-assisted breeding approaches. Peter Gresshoff (University of Tennessee, USA) showed the usefulness of DNA

amplification fingerprinting (DAF) in the generation of appropriate markers; DAF technique results in highly reproducible profiles in soybean. (See *Probe* 4 (3/4):32-36)

Graphical Representation of QTLs

The Maize Workshop focused on the theme of reporting, displaying, and utilizing complex data from quantitative trait loci (QTL) studies. Ed Coe (USDA, Columbia, USA) commented on the crucial importance of integrating quantitative trait information with molecular genetic data in working toward the goal of understanding the structure and function of the maize genome, and applying this information. Diego Gonzalez de Leon from the Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT, Mexico) showed methods for concise graphic representation of QTL results across different traits and environments. When using QTL data in marker-assisted selection (MAS) at CIMMYT, Gonzalez' group takes into account the size and effects of QTL regions, as well as economic thresholds that must be targeted.

Mathilde Causse from the Institut National de la Recherche Agronomique (INRA, France) explained research underway in her unit on using QTL methodology to understand early growth, carbon metabolism, drought tolerance, and variation in protein quantities in maize. She explained her location's in-house database, which has numerous options for managing and visualizing QTL data. Clare Nelson (Cornell University, USA) demonstrated QGENE, a software package he developed for analyzing and viewing QTL data and for applying such data to MAS. Pat Byrne (USDA, ARS, Columbia, USA) provided an on-line demonstration of accessing and searching QTL information in USDA's Maize Genome Database.

Mapping and Tagging Genes

A workshop on mapping and tagging abiotic stress genes, including drought resistance, water stress, high temperature, winter hardiness and salinity tolerance, identified the genetic complexity of these traits and the laborious mission of traditional plant breeding. Henry Nguyen, John Mullet, and their colleagues at Texas Tech (USA) and Texas A&M Universities (USA) have tagged the "stay green" gene, a post-flowering drought-resistant QTL in sorghum, by using molecular markers. Three major regions on the chromosome have been found to control the stay green trait in different environments. This trait is also linked to enhanced nicotinamide adenine dinucleotide phosphate (NADP) reducing power, higher chlorophyll content and increased NADP malic enzyme activity. In addition to relieving drought stress in sorghum, the stay green gene may have application in improving turf grasses.

Inventory of Expressed Genes in Plants

The *Arabidopsis* Sequencing Project (Michigan State University, USA) is generating approximately 1,000 Expressed Sequence Tags (ESTs) per month. These ESTs provide not only a new source of very useful molecular markers but cDNAs also can be used to constitute a genetic map of expressed genes. Anonymous cDNA clones randomly selected from cDNA libraries of roots, etiolated seedlings, leaves, stems and flowering structures and from various developmental stages were sequenced. Thomas Newman (Michigan State University, USA) reported that approximately 35 percent of the ESTs show significant similarities to previously characterized genes in the public databases from plant and non-plant organisms.

The use of EST technology permits the rapid identification of new coding regions in plant genes, especially those whose isolation would otherwise be difficult or impossible. Plant biologists can directly use knowledge about proteins and genes from non-plant sources. Newman expects that tens of thousands of *Arabidopsis* ESTs will be deposited in the public databases during the next several years. Marc van Montagu (Ghent, Belgium) announced the addition by the European consortium of 4,500 ESTs to the public databases through November 1994.

In addition to the *Arabidopsis* program, the Japanese Rice Genome Program (Tsukuba, Japan) has developed rice libraries from calli, root, shoot, and developing seeds, and has generated approximately 20,000 analyzed cDNAs. Craig Venter (The Institute for Genome Research(TIGR), USA) presented results of sequencing ESTs from human cDNA libraries as an approach to quickly finding new genes. This strategy results in a tripled rate of new gene identification in both

human and plant species. TIGR scientists are currently sequencing approximately a half-million base pairs of DNA per day and expect to analyze 35,000 new ESTs by the end of 1995. The Expressed Gene Anatomy Database (EGAD) was developed to integrate DNA sequences and mapping data with corollary biological information as gene expression, biochemical function, or cellular role.

Plant Gene Nomenclature

Ellen Reardon and Carl Price (Rutgers University, USA) organized a workshop focusing on the challenges in collection, collation and dissemination of nomenclature for sequenced plant genes. Nomenclature of genes across the plant kingdom is based primarily on the function of the gene products and secondarily on sequence similarity.

Brian Smith-White (Michigan State University, USA) related that the application of appropriate nomenclature to related sequences provides the framework for bringing order out of chaos. Smith-White's shibboleth in applying new terminology is "be conservative." Copies of genes encoding proteins of similar function exist in organelles and in the nucleii of many plants. David Lonsdale (Norwich, UK) discussed the potential for problems replacing terms that no longer convey current understanding. Specifically, the replacement of nads and ndhs with nuos in chloroplast, mitochondrial or *E. coli* genomes offered an opportunity to establish common nomenclatures across multiple genomes.

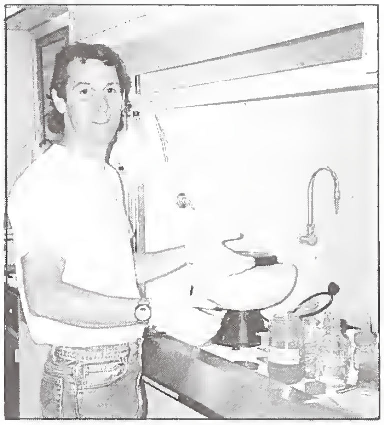
Paul Staswick (University of Nebraska, USA), associate editor of *Plant Physiology*, addressed the problem of converting gene designations in submitted publications to the common nomenclature. Authors would be encouraged to use the common nomenclature, but no worthwhile paper would be rejected for failure to do so.

Finally, Doug Bigwood, (NAL, USDA, Beltsville, USA) announced that CPGN databases are available on the World Wide Web at: http://probe.nalusda.gov:8300.html

An approved gene name can provide the springboard to identifying the location of specific loci across the plant kingdom. ◆

Reprinted from Plant Molecular Biology Report (1995) 13(1): 63-69

Introducing Dr. David B. Neale



Dr. David Neale is a Plant Molecular Geneticist at the Institute of Forest Genetics, Pacific Southwest Research Station, USDA Forest Service, a position he has held since 1986. Working in Albany and Placerville, California, Dr. Neale directs the Institute's basic research program on forest tree genomes, and collaborates with a variety of research organizations and universities.

Dr. Neale's specific area of research is the molecular biology of western conifers, a subject on which he has published extensively. He is most interested in the woody perennials' genetics as they relate to wood development, adding that "their large size and long generation times make them difficult organisms to study."

In addition to his work with the Forest Service, Dr. Neale is an adjunct professor at the University of California, Davis, the institution where he completed a postdoctoral fellowship in 1986. His research there included oats and barley as well as conifers.

A native of Connecticut, Dr. Neale's doctoral studies took him out to the west coast. He received his Ph.D. in Forest Genetics from Oregon State University in 1984. His M.S. degree in Forest Genetics, received in 1978, is from the University of New Hampshire, the same institution from which he received a B.S. in Forest Science in 1976. Contact Dr. David Neale at: PHONE: (510) 559-6436, FAX: (510) 559-6499, EMAIL: dbnEs27wO07.pswfs.gov ◆

Flow Cytometry and Genome Analysis

J.S. (Pat) Heslop-Harrison
Department of Cell Biology
John Innes Centre
Colney Lane, Norwich NR4 7UH
United Kingdom

Flow cytometry allows for fast and informative, quantitative and qualitative analysis of objects including chromosomes and nuclei, normally by measuring the fluorescence of molecules that are specifically bound to structures of interest (figure 1; Melamed *et al*., 1990). The molecules measured are often fluorochrome-conjugated antibodies or fluorescent dyes binding specifically to DNA or proteins.

Flow cytogenetics underpins much of the human genome project: the Department of Energy Human Genome Program reports that "among the resources most crucial to mapping progress are the libraries of clones representing each of the human chromosomes. This chromosome-specific clone library production from physically purified chromosomes depends on the unique chromosome-sorting facilities" at Los Alamos and Lawrence Livermore National Laboratories (Anon, 1993). Flow technology is also recognized as being critical to pig and bovine genome projects (Miller *et al*., 1992; Dixon *et. al*., 1992).

Joe Gray, from the University of California, San Francisco, and Scott Cram, Life Science Division Leader at Los Alamos Natonal Laboratory, described some of the advantages of flow cytometry for plant molecular cytogenetics and genome analysis. "The analysis and sorting of plant chromosomes is of considerable economic interest. As is the case for mammalian chromosomes, flow karyotyping and chromosome sorting provide the opportunity for gene mapping and the construction of chromosome-specific libraries" (Gray and Cram, 1990).

Developments

Since they wrote this, there have been successful applications of the methods in plants for genome size measurements (including the specific AT and GC base-pair content), cell cycle analysis, flow karyotyping (by measuring the DNA content of chromosomes), chromosome sorting and production of chromosome-enriched DNA libraries, although these analyses are not as yet extensively exploited.

In this short review, I aim to highlight potential and recent applications of flow cytometry to plant genomes; the literature on chromosome analysis has been reviewed recently by a group of European collaborators from the Czech Republic, Italy and Germany (Dolezel *et al*. 1994), while many techniques for flow analysis of plants are discussed in the same paper and elsewhere (e.g., Heslop-Harrison and Schwarzacher, 1995).

Genome size analysis - Changes between species, during differentiation and during the cell cycle

Analytical information about the physical size of plant genomes and their state of replication is easily obtainable from flow cytometry. Knowing the number of base pairs in a genome is valuable for studies of new species, and an extensive list based on flow cytometric estimates was published by Aru Arumuganathan, now at the University of Lincoln, Nebraska, and Lisa Earle, from Cornell University, in 1991.

Flow cytometry provides a fast and accurate way to look at changes

Probe

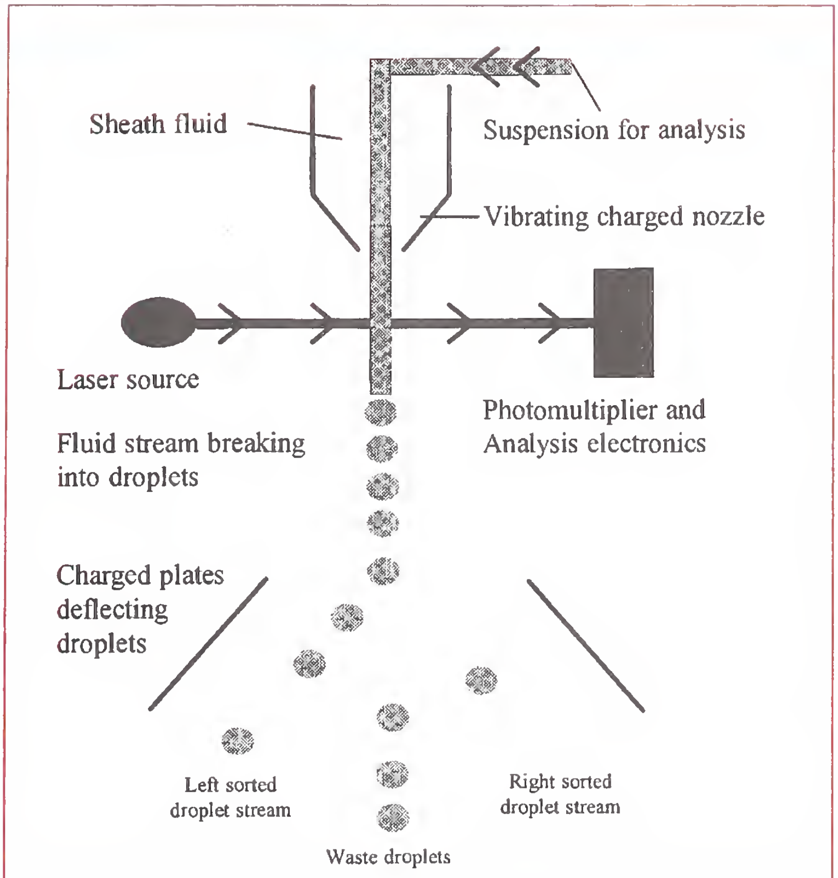


Figure 1. The optical and mechanical arrangement of a flow cytometer capable of measuring the fluorescence of stained particles, such as chromosomes or nuclei, in a fluid stream. After measurement, the particles, by now contained in droplets, are sorted by charged plates depending on their fluorescence.

in genome size during evolution and differentiation. Establishment of ploidy and aneuploidy changes during tissue culture, and examination of intra- and inter-specific variation of DNA content can all be important in plant hybridization, breeding, and genetic manipulation programs (Dolezel *et al.* 1994; Leitch *et al.* 1992). Perhaps, in contrast to animals, polyploidy often accompanies differentiation, and is an important part of plant development, with different cell types having characteristic ploidies (Galbraith *et al.* 1991; Bino *et al.* 1993). Such differentiation by polyploidization is important for understanding the regulation of gene expression in differentiated tissues, and for understanding the nature of tissues used for plant regeneration and transformation.

Flow cytometry provides an accurate method for determining the proportions of cells in G1, S and G2/M stages of the cell cycle. These data can be used to calculate cell cycle times, which are needed in studies of the genetics and control of this process, and are useful for analysis of aspects of crop growth and development.

Flow karyotyping

Flow karyotypes, giving the average sizes of chromosomes from mitotic cells, are quick, accurate and quantitative. To make a flow karyotype, a suspension of many thousands of chromosomes is made and stained with a fluorochrome which binds quantitatively to DNA. The fluorescence of chromosomes is measured as they pass individually through a cytometer, giving a histogram (figure 2) where each peak represents one or a group of chromosomes. Flow methods enable differences as small as 1.5 to 4 Mb to be analyzed in humans, and both aneuploidy and many chromosome deletions can be detected easily. In plants, eight species have been flow karyotyped so far (see Dolezel *et al.* 1994), including *Haplopappus gracilis*, a plant with only two pairs of chromosomes, four solanaceous species and *Melandrium album* (with sex chromosomes), wheat (*Triticum aestivum*), and field or broad bean (*Vicia faba*).

Chromosome sorting for gene mapping and library construction

After identification of a chromosome by its fluorescence, particular chromosomes can be sorted from others in a flow cytometer by either electrical (as in figure 1) or mechanical deflection. Chromosome sorting has been achieved from important crop species including wheat, tomato (*Lycopersicon esculentum*), and field bean. Sorted chromosomes serve as a source of DNA for production of chromosome-specific and chromosome-recombinant DNA libraries. A chromosome-specific recombinant

Probe

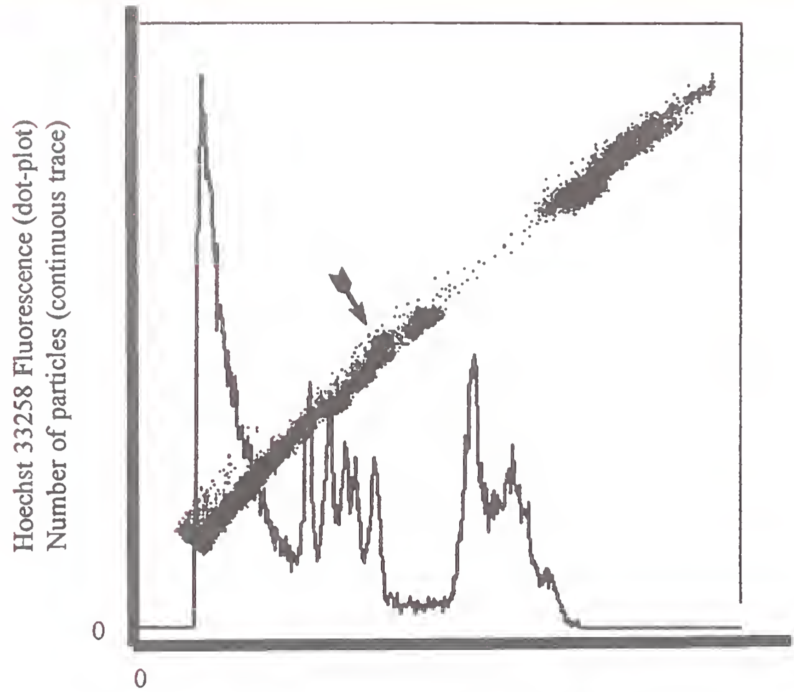


Figure 2: A "flow karyotype" of a wheat cell line. The continuous trace is a frequency distribution histogram showing the number of chromosomes with each particular fluorescence. The five sharp peaks correspond to single chromosomes or pairs of chromosomes, while the smoother curves are formed where many individual chromosome types are not resolved (right), or from broken chromosomes, nuclei, and organelles (left). This graph is derived from a two-wavelength analysis, shown as the diagonal line where density of dots is proportional to number of chromosomes detected of each fluorescence. Some peaks on the continuous line are now resolved as two peaks (arrow). The karyotype is derived from analysis of 50,000 chromosomes, taking about 5 minutes. I thank Nigel Miller at the Babraham Institute, Cambridge, for assistance in operating the flow cytometer.

DNA library from chromosome 4A showed 20-fold enrichment of clones as compared to a random genomic library (Wang *et al.* 1992). Partitioning the genome before cloning can reduce the effort required for screening a library.

Dot blots, in which chromosomes are sorted onto membranes, have been used for gene mapping by probing with cDNA and other clones. Primers for the polymerase chain reaction (PCR) can be mapped by using sorted chromosomes as the DNA source (Macas *et al.* 1993), and subchromosomal localization is possible by probing sorted chromosomes from karyotypes with translocations. Sorted chromosomes also can be used for microinjection, bombardment, or electroporation into regenerable tissues to make, perhaps, chromosome-specific transfectants.

Quantification

Flow cytometry can be used to measure small DNA molecules -- down to 20 kb, below the threshold of separation by normal electrophoresis. The ability to quantify accurately large (from 20 kb to chromosomal size) DNA molecules may be useful in analysis of large genomic features -- the distibution of *Not*I or *Mlu*I islands, for example. Work at National Flow Cytometry Resource Center, Los Alamos, and elsewhere, is pushing the limits to base-pair resolution: DNA sequencing at rates of tens of base pairs per second may be feasible by *Bal* 31 exonuclease digestion of a single DNA molecular and cytometric identification of the bases as they are cut off. *In situ* hybridization methods in suspension may enable accurate quantification of numbers of copies of repetitive DNA sequences on different chromosomes in a species -- something often difficult to do by other methods.

Conclusions

Applications of flow cytogenetics range from detection of aberrant cell cycles and changes in nuclear DNA amounts to sorting of chromosomes for gene mapping and library construction. The methods are used extensively in the human genome project, and are applicable to plants. The fast and quantitative results make the method an important analytical tool which has the potential to advance many aspects of plant genome analysis.

Anon 1993. 1991-1992 Department of Energy Human Genome Program, Los Alamos National Laboratory, Gene Library Project Report.

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important plant species *Plant Mol Biol Reporter* **9**: 208-218.

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Gray JW, Cram LS. 1990. Flow karyotyping and chromosome sorting. In: *Flow Cytometry and Sorting*. New York: Wiley Liss, 503-529.

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Arabidopsis Workshop at PGIII, January 17, 1995, San Diego, USA

Dr. Mary Anderson, Director
The Nottingham Arabidopsis *Stock Center*
School of Biological Sciences
University of Nottingham, United Kingdom

The *Arabidopsis* workshop focused on the more global aspects of *Arabidopsis* research, looking at progress in the mapping and sequencing of the genome.

Renate Schmidt (John Innes Centre, UK) presented a progress report on the physical mapping of chromosomes 4 and 5 by the Dean Group. Using 140 markers in hybridization experiments on the 4 available YAC libraries, in combination with chromosome- walking, they have managed to generate eight contigs which span chromosome 4. Current estimates on the size of this chromosome are around 20.5 Mb. The position of the centromere and the rDNA have been identified.

Schmidt reported that repeated DNA around the centromere proves problematic in the chromosome-walking experiments, as some tandemly repeated sequences localized in the centromeric region are likely to be lost from the YAC inserts following replication. Good progress was also reported for chromosome 5, which now is covered by 40 contigs.

Bertrand Lemieux (York University, Canada) presented an

overview of his EST mapping project. He described the use of a PCR-based approach to identifying YACs which contain a limited set of ESTs from the NCBI repository. This work is being done in collaboration with Ron Davis at Stanford (USA), the French *Arabidopsis* genome mapping group and Joe Ecker at Penn State (USA). The YAC libraries being used are the CIC and the yUP banks with a few EG clones included. So far 600 primers and 140 ESTs have been used to anchor 192 YAC clones.

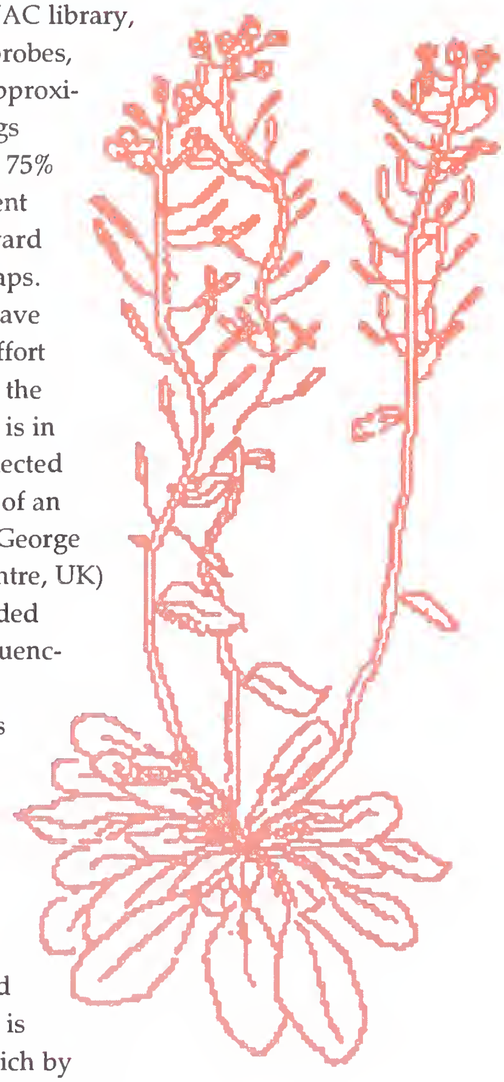
Tom Newman (Michigan State, USA) reported on the progress of the MSU *Arabidopsis* cDNA project. The group's goal is to generate Expressed Sequence Tags (ESTs) for about 85% of the expressed genes in this model system. This effort complements the French cDNA sequencing initiative reported on at one of the main sessions. The MSU group is now sequencing approximately 1,000 ESTs per month and has already deposited 10,000 ESTs in dbEST at NCBI. Sequence analysis before submission to dbEST is conducted through a collaboration with Ernie Retzel's Biocomputing Group at Minnesota.

Clones and libraries are available from the *Arabidopsis* Biological Resource Center at Ohio State (USA). The generation of a subtracted library is a major priority. Newman reported that all the clones from which ESTs have been generated will be removed from the cDNA library so that low abundance cDNAs can be identified.

Howard Goodman (Massachusetts General Hospital, Boston, USA) reported on progress of mapping chromosome 2. Using anchored markers, the new CIC YAC library, and walking with end-probes, they have established approximately eight YAC contigs covering approximately 75% of chromosome 2. Current efforts are directed toward closing the remaining gaps.

In addition, they have initiated a sequencing effort on chromosome 2 using the multiplex method. Data is in the process of being collected on four cosmids as part of an initial feasibility study. George Murphy (John Innes Centre, UK) reported on the EU-funded European Scientists Sequencing *Arabidopsis* (ESSA) program which involves seven laboratories across the EU which aim to sequence a contiguous region of 2 million bases of chromosome 4 of *Arabidopsis* over a period of 3 years. The program is coordinated from Norwich by Mike Bevan, and about 40% of the sequencing will be performed there.

Analysis of the first two cosmids sequenced in Norwich shows that the gene density is about one gene every 5 kb. Interestingly, although a number of computing techniques were applied to identify coding regions, none were able to detect two genes eventually located by hybridization of a cDNA library to the cosmids. ◆



Coming Next Month

Plant Chromosomes at High Resolution

Bacterial Artificial Chromosome Libraries for Genome Analysis

Announcing The Journal of Quantitative Trait Loci

Calendar of Upcoming Genome Events

MEETINGS 1995

May 21-25: **American Society of Biochemistry & Molecular Biology Conference, San Francisco, CA.** Contact: Nancy Sledge, 9650 Rockville Pike, Bethesda, MD 20814. VOICE: (301) 530-7010, FAX: (301) 530-7014.

May 22-24: **22nd Stadler Genetics Symposium: Genomes; Launch Pad for Discovery, Columbia, MO.** Contact: Dr. Perry Gustafson, VOICE: (314) 882-7318, FAX: (314) 875-5359, EMAIL: agro1375@mizzou1.missouri.edu

May 24-26: **Seventh Annual National Agricultural Biotechnology Council Meeting: Genes for the Future: Discovery, Ownership, Access, Columbia, MO.** Contact: National Agricultural Biotechnology Council, 159 Biotechnology Bldg., Cornell University, Ithaca, NY 14853-2703.

May 28-June 3: **10th International Congress on Nitrogen Fixation, St. Petersburg, Russia.** Contact: Prof. I. Tikhonovich, Congress Organizer to the National Organizing Committee, Research Institute for Agricultural Microbiology, P.B. 364, General Post Office, 190000, St. Petersburg, Russia. FAX: (812) 470-43-62, EMAIL: chief@riam.spb.su.

June 4-9: **Second Latin American Meeting on Plant Biotechnology, Puerto Iguazu, Argentina.** Contact: Dr. Alejandro Mentaberry, Southern Cone Coordinator, INGEBI-CONICET, Obligado 2490, 1428 Buenos Aires, Argentina. FAX: 55 1 786 8578.

June 5-7: **Bioinformatics, San Francisco, CA.** Contact: Cambridge Healthtech Institute, 1000 Winter St., Suite 3700, Waltham, MA 02154. VOICE: (617) 487-7989, FAX: (617) 487-7937.

June 10-13: **Value-Added Cereals Through Biotechnology, Saskatoon, Canada.** Contact: Rosemarie Gallays, Information Officer, National Research Council Canada, Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, Saskatchewan, Canada S7N 0W9. VOICE: (306) 975-5571, FAX: (306) 975-4839.

June 11-16: **Gordon Research Conference: Biological Structure and Gene Expression, Newport, RI.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

June 11-16: **Gordon Research Conference: Plant Cell Genetics and Development, Wolfeboro, NH.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

June 11-16: **Gordon Research Conference: Genetic Toxicology, New London, NH.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

June 11-16: **Gordon Research Conference: Nucleic Acids, New Hampton, NH.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

June 18-23: **American Chemical Society, Division of Agrochemicals Special Conference VI: Molecular Genetics and Ecology of Pesticide Resistance, Big Sky, Montana.** Contact: American Chemical Society, Dept. of Meetings, Expositions and Divisional Activities, 1155 Sixteenth St. NW, Washington, DC 20036. VOICE: (202) 872-6286, FAX: (202) 872-6128.

June 18-23: **Gordon Research Conference: Biological Regulatory Mechanisms, Plymouth, NH.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

June 18-23: **Gordon Research Conference: Proteins, Tilton, NH.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

MEMO

Dear Readers:

Your interests are important to us. Articles and news items are welcome.

Next deadline: July 14, 1995

Editor

June 25-28: **Agri-Food Quality '95: Interdisciplinary Opportunities and Objectives for the Year 2000 and Beyond, Norwich, UK.** Contact: Agri-Food Quality '95, Institute of Food Research, Norwich Research Park, Colney, Norwich NR4 7UA, UK. VOICE: +44 (0) 603 255000, FAX: +44 (0) 603 507723.

June 25-30: **Gordon Research Conference: Developmental Biology, Andover, NH.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

June 25-30: **Gordon Research Conference: Lipid Metabolism, Meriden, NH.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

June 26-30: **Seventh International Conference of Conifer Biotechnology Working Group, Queensland, AU.** Contact: Prof. R.D. Teasdale, ForBio Research, 50 Meiers Rd., Indooroopilly, Qld 4068, Australia.

July 2-7: **Gordon Research Conference: Plasmid and Chromosome Dynamics, Plymouth, NH.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

July 4-7: **9th International Rapeseed Congress, Cambridge, England.** Contact: Denis Kimber, 44 Church St., Haslingfield, Cambridge, CB3 7JE, England.

July 8-12: **Protein Society Symposium, Boston, MA.** Contact: Nancy Sledge, Exhibits Manager, FASEB, 9650 Rockville Pike, Bethesda, MD 20814. VOICE: (301) 530-7009, FAX: (301) 530-7014.

July 9-14: **Gordon Research Conference: Molecular Membrane Biology, Andover, NH.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

July 14-19: **15th International Conference on Plant Growth Substances, Minneapolis, MN.** Contact: Gary Gardner, Dept. of Horticultural Science, University of Minnesota, 305 Alderman Hall, St. Paul, MN 55108. FAX: (612) 624-3606, EMAIL: ggardner@maroon.tc.umn.edu

July 16-21: **Gordon Research Conference: Enzymes, Coenzymes and Metabolic Pathways, Meriden, NH.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

July 17-21: **4th International Symposium on the Molecular Biology of the Potato, Wageningen, The Netherlands.** Contact: IAC-Section OCC, P.O. Box 88, 6700 AB Wageningen, The Netherlands. VOICE: 31-8370-90232, FAX: 31-8370-18552.

July 23-38: **Gordon Research Conference: Plant and Fungal Cytoskeleton, Andover, NH.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

July 29-August 2: **American Society of Plant Physiologists Annual Meeting, Charlotte, NC.** Contact: Susan Chambers, Director of Finance and Administration, 15501 Monona Dr., Rockville, MD 20855-2768. VOICE: (301) 251-0560 ext. 11, FAX: (301) 279-2996, EMAIL: chambers@access.digex.net

July 30-August 8, **1996: Oat Conference/Barley Genetics Symposium, Saskatoon, Canada.** Contact 5th IOC and 7th IBGS 1996, Crop Development Centre, University of Saskatchewan, Saskatoon, Canada, S7N 0W0. FAX: (306) 966-5015. Symposiums will be held concurrently.

July 31-August 4: **14th General Congress of the European Association for Research on Plant Breeding (EUCARPIA), Jyvaskkyla, Finland.** Contact: Prof. Peter M.A. Tigerstedt, University of Helsinki, Division of Plant Breeding, Viikki D-talo, 00710, Helsinki, Finland.

August 3-5: **Penn State's 14th Summer Symposium in Molecular Biology: Chromosomal Controls of Gene Expression, University Park, PA.** Contact: Kamal Rashid, Symposium Director, Penn State Biotechnology Institute, 519 Wartik Lab., University Park, PA 16802. VOICE: (800) 833-5533, FAX: (814) 863-1357.

August 6-12: **20th World Congress of the International Union of Forestry Research Organisations: Caring for the Forest; Research in a Changing World, Tampere, Finland.** Contact: IUFRO-95 Congress Secretariat, Finnish Forest Research Institute, Unioninkatu 40 A, FIN-00170 Helsinki, Finland. VOICE: +358-0-857 051, FAX: +358-0-625 308, TELEX: 121286 metla sf, EMAIL: iufro95@metla.fi

August 13-18: **Gordon Research Conference: Epigenetics, Plymouth, NH.** Contact: Gordon Research Conferences, University of Rhode Island, P.O. Box 984, West Kingston, RI 02892-0984. VOICE: (401) 783-4011, FAX: (401) 783-7644, EMAIL: grc@grcmail.grc.uri.edu.

August 20-25: **International Poplar Symposium, Seattle, WA.** Contact: Continuing Education (Poplar), College of Forest Resources, University of Washington, AR-10, Seattle, WA 98195. VOICE: (206) 543-0867, FAX: (206) 685-0790, EMAIL: carkey@u.washington.edu.

August 29-31: **50th Society for Experimental Biology Symposium, Unifying Plant Genomes: Comparisons, Conservation and Colinearity, Cambridge, UK.** Contact: Dr. J.S. Heslop-Harrison, John Innes Centre for Plant Science Research, Colney Lane, Norwich, NR4 7UH, England. FAX: +44-0-603-52571, EMAIL: hharrison@afrc.ac.uk.

October 1-4: **Engineering Plants for Commercial Products/Applications, Lexington, KY.** Contact: International Symposium on Engineering Plants, c/o Conferences and Institutes, 218 Peterson Service Bldg., Lexington, KY 40506-0005. VOICE: (606) 257-3929, FAX: (606) 323-1053, EMAIL: monica.stoch@ukwang.uky.edu

October 16-20: **Third International Rice Genetics Symposium, IRRI, Philippines.** Contact: Dr. G.S. Khush, International Rice Research Institute, P.O. Box 933, Manila, Philippines.

October 22-25: **Third New Crops Symposium, Indianapolis, IN.** Contact: Jules Janick, Indiana Center for New Crops and Plant Products, Purdue University, 1165 Horticulture Bldg., West Lafayette, IN 47907-1165. FAX: (317) 494-0391.

WORKSHOPS AND COURSES 1995

May 13-15: **PCR Techniques, Washington, DC.** Contact: Director, Center for Advanced Training in Cell and Molecular Biology, Catholic University of America, 620 Michigan Ave., NE, Washington, DC 20064. VOICE: (202) 319-6161, FAX: (202) 319-4467, EMAIL: millerm@cua.edu.

May 14-19: **Advanced Course on Plant Biotechnology Workshop, Leiden, Netherlands.** Contact: Dr. Ir. L.A. van der Meer-Lerk, Kluyver Laboratory, Julianalaan 67, 2628 BC Delft, Netherlands. VOICE: (015) 785 140, FAX: (015) 782 355.

May 15-19: **Basic Cell and Tissue Culture, Washington, DC.** Contact: Director, Center for Advanced Training in Cell and Molecular Biology, Catholic University of America, 620 Michigan Ave., NE, Washington, DC 20064. VOICE: (202) 319-6161, FAX: (202) 319-4467, EMAIL: millerm@cua.edu.

May 16-19: **DNA Sequencing, Washington, DC.** Contact: Director, Center for Advanced Training in Cell and Molecular Biology, Catholic University of America, 620 Michigan Ave., NE, Washington, DC 20064. VOICE: (202) 319-6161, FAX: (202) 319-4467, EMAIL: millerm@cua.edu.

May 31-June 3: **Site Directed Mutagenesis, Washington, DC.** Contact: Director, Center for Advanced Training in Cell and Molecular Biology, Catholic University of America, 620 Michigan Ave., NE, Washington, DC 20064. VOICE: (202) 319-6161, FAX: (202) 319-4467, EMAIL: millerm@cua.edu.

June 5-9: **Plant Biotechnology, Plant Gene Transfer,** and **Plant Gene Expression, Washington, DC.** Contact: Director, Center for Advanced Training in Cell and Molecular Biology, Catholic University of America, 620 Michigan Ave., NE, Washington, DC 20064. VOICE: (202) 319-6161, FAX: (202) 319-4467, EMAIL: millerm@cua.edu.

June 19-30: **An International Training Program in New Crops: Medicinal and Aromatic Plants, West Lafayette, IN.** Contact: Tom Robertson, Attn: International Training Program in Aromatic and Medicinal Plants, Continuing Education, Purdue University, 1586 Stewart Center, West Lafayette, IN 47907-1586. VOICE: (317) 494-7220, FAX: (317) 494-0567.

July 3-8: **DNA-Binding Proteins & Transcriptional Regulators, Washington, DC.** Contact: Director, Center for Advanced Training in Cell and Molecular Biology, Catholic University of America, 620 Michigan Ave., NE, Washington, DC 20064. VOICE: (202) 319-6161, FAX: (202) 319-4467, EMAIL: millerm@cua.edu.

July 10-14: **Recombinant DNA Methodology, Washington, DC.** Contact: Director, Center for Advanced Training in Cell and Molecular Biology, Catholic University of America, 620 Michigan Ave., NE, Washington, DC 20064. VOICE: (202) 319-6161, FAX: (202) 319-4467, EMAIL: millerm@cua.edu.

July 17-21: **Protein Purification and Analysis, Washington, DC.** Contact: Director, Center for Advanced Training in Cell and Molecular Biology, Catholic University of America, 620 Michigan Ave., NE, Washington, DC 20064. VOICE: (202) 319-6161, FAX: (202) 319-4467, EMAIL: millerm@cua.edu.

August 6-11: **10th International Workshop on Plant Membrane Biology, Regensburg, Germany.** Contact: Widmar Tanner, Lehrstuhl für Zellbiologie und Pflanzenphysiologie, Universität Regensburg, Universitätsstrasse 31, 93053 Regensburg, Germany. FAX: 49-941-943-3352.

August 24-29: **1997: 17th International Congress for Biochemistry and Molecular Biology, San Francisco, CA.** Contact: Congress Secretariat, 17th International Congress for Biochemistry and Molecular Biology, 9650 Rockville Pike, Bethesda, MD 20814-3996. FAX: (301) 571-1824, EMAIL: 171UBMB@asbmb.faseb.org.

August 29-31: **Society for Experimental Biology Annual Meeting, Cambridge, England.** Contact: Society for Experimental Biology, Burlington House, London W1V 0LQ, United Kingdom. VOICE: 44 171 439 8732, FAX: 44 171 287 4786.

September 1-3: **ITMI International Public Workshop, Norwich, England.** Contact: International Triticeae Mapping Initiative, Management Office, Genetic Resources Conservation Program, University of California, Davis, CA 95616-8602. VOICE: (916) 757-8920, FAX: (916) 757-8755, EMAIL: itmi@ucdavis.edu

August 3-5: **Penn State's 14th Summer Symposium in Molecular Biology: Chromosomal Controls of Gene Expression, University Park, PA.** Contact: Kamal Rashid, Symposium Director, Penn State Biotechnology Institute, 519 Wartik Lab., University Park, PA 16802. VOICE: (800) 833-5533, FAX: (814) 863-1357.

October 1-4: **Engineering Plants for Commercial Products/Applications, Lexington, KY.** Contact: International Symposium on Engineering Plants, c/o Conferences and Institutes, 218 Peterson Service Bldg., Lexington, KY 40506-0005. VOICE: (606) 257-3929, FAX: (606) 323-1053, EMAIL: monica.stoch@ukwang.uky.edu

October 13-14: **Workshop on Gene-Finding and Gene Structure Prediction, Philadelphia, PA.** Contact: David Searls, Dept. of Genetics, CRB475, University of Pennsylvania School of Medicine, 422 Curie Blvd., Philadelphia, PA 19104-6145. VOICE: (215) 573-3107, FAX: (215) 573-3111, EMAIL: dsearls@cbil.humgen.upenn.edu.

Whats New...

The Plant Genome calendar of events is now on gopher and updated monthly.

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Plant Genome Publications

The following publications are available. If you would like to receive a copy, check off the title and mail your request to:

Plant Genome Data and Information Center
National Agricultural Library, ARS, USDA
10301 Baltimore Blvd., 4th Floor
Beltsville, MD 20705-2351

CRIS/ICAR Projects and Bibliographies:

The sponsored research projects were obtained by searching CRIS/ICAR (USDA and CARC, North America) using AGRISEARCH Silver Platter CD. Bibliographies were obtained by searching AGRICOLA Silver Platter CD.

DNA Fingerprinting and Plants. November 1994. Compiled by Andrew Kalinski.

Gene Tagging in Plants. December 1994. Compiled by Andrew Kalinski.

Molecular Markers in Plant Genome Analysis. December 1994. Compiled by Andrew Kalinski.

Transgenic Cotton. December 1994. Compiled by Andrew Kalinski.

Transgenic Wheat. December 1994. Compiled by Andrew Kalinski.

Transposable Elements in Plants. December 1994. Compiled by Andrew Kalinski.

Miscellaneous Publications:

Prepared by the Biotechnology Information Center staff.

AG/Biotechnology Electronic Information.

ALF (Agricultural Library Forum): The National Agricultural Library's Electronic Bulletin Board System -- Brief Guide. Prepared by Karl Schneider

Biotechnology Directories.

Databases Pertaining to Biotechnology.

Guide to Information Sources in Biotechnology.

Newsletters Pertaining to Agricultural Biotechnology

List of Molecular Biology E-mail Servers. Prepared by Amos Bairoch, Dept of Medical Biochemistry, University of Switzerland.

Other Informational Products:

Prepared by the Genome Informatics Group.

Plant Genome Database CD-ROM

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